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Genome sequencing project has begun on two plant trypanosomatids (“*Phytomonas*”).

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Some trypanosomatids are responsible for wilt in tropical crops, such as hartrot disease in the coconut palm. They have a major economic impact in Latin America and the Caribbean. In the latex vessels of some plants, other trypanosomatids appear to be “symbiont-like”, without any negative effect on their host, and others multiply in fruits and seeds. The latter usually belong to the genera *Crithidia*, *Herpetomonas* and *Leptomonas,* formerly known as “lower trypanosomatids”. Only one arbitrary genus name has been proposed as yet for all these trypanosomatids living in plants, in different tissues, with different consequences: “*Phytomonas*”. After the Trytrip project and the recent discovery of lower trypanosomatids in immuno-suppressed patients, it became increasingly interesting to compare genome sequences outside *Trypanosoma* and *Leishmania* in order to better understand the molecular evolutionary relationships within the protozoan order Kinetoplastida.

In 2008, the French National Research Agency (ANR) decided to sponsor a project on the sequencing of two plant trypanosomatids, one -Hart 1, group H - responsible for a disease of coconut (hartrot) in Latin America, and non-pathogenic one –EM1, group D - from Euphorbia in France.

Sequencing of the isolates was performed using data from three different technologies (454 Titanium, Illumina GAIIx and Sanger). Assemblies obtained by Newbler (Roche) showed high continuity. We also obtained cDNA sequences using 454 Titanium to help annotation. The assemblies were of sufficient continuity to start an automatic annotation phase, using procedures that involve cDNA, matches to protein data, and de novo gene finding.

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